

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 1999, 08:14:24 ; Search time 14.51 Seconds

(without alignments)
492.984 Million cell updates/sec

Title: US-09-193-881-23

Perfect score: 1622

Sequence: 1 MCAERLQGFMTALVATFD.....GPSGSEWEDQSESDIR 302

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1271	78.4	251	1 R97978	Stannocalcin alpha
2	354	21.8	247	1 R84522	Stannocalcin from
3	351.5	21.7	261	1 P82968	Corpuscles of Stan
4	97	6.0	648	1 R22561	Mouse mutant c-ra
5	97	6.0	648	1 R22563	Mouse mutant c-ra
6	97	6.0	648	1 R22560	Mouse mutant c-ra
7	96.5	5.9	648	1 R22562	Mouse mutant c-ra
8	96.5	5.9	693	1 W15140	Mouse mutant c-ra
9	96.5	5.9	1038	1 W19766	Mammalian cell c
10	92	5.7	457	1 W19766	Mouse interleukin
11	92	5.7	542	1 W73633	Human secreted pro
12	91	5.6	648	1 W36344	Human secreted pro
13	91	5.6	648	1 R22559	Mouse c-ra-1, Det
14	91	5.6	648	1 W17046	Mutant mouse c-ra
15	91	5.6	648	1 W17047	Mutant mouse c-ra
16	91	5.6	648	1 W17048	Mutant mouse c-ra
17	91	5.6	648	1 W17049	Mutant mouse c-ra
18	91	5.6	648	1 W17045	Mutant mouse c-ra
19	91	5.6	648	1 W30668	Mouse c-ra-1 prot
20	91	5.6	648	1 W30665	Mutant mouse c-ra
21	91	5.6	648	1 W30665	Mutant mouse c-ra
22	91	5.6	648	1 W30665	Mutant mouse c-ra
23	86	5.3	2189	1 R05222	Antigen GX5401F e
24	84.5	5.2	598	1 R33552	Sequence of splice
25	84.5	5.2	571	1 R39565	Human neuronal VDC
26	84.5	5.2	598	1 R72612	Human calcium chan
27	84.5	5.2	598	1 W63144	Human calcium chan
28	84	5.2	340	1 W17081	EPH family ligand
29	84	5.2	340	1 W46615	Human transmembran
30	84	5.2	1301	1 W92296	Human alpha-1 (XVI
31	83	5.1	648	1 R98215	Human Raf1 kinase
32	83	5.1	648	1 W13107	Human Raf-1, Compl
33	83	5.1	648	1 W10637	NHERF2 ligand for
34	83	5.1	648	1 W17044	Human c-ra-1 prot
35	83	5.1	340	1 W13544	Human cytokine ler
36	83	5.1	455	1 W33698	AL-2-long (AL-21)
37	83	5.1	340	1 W33698	AL-2-short (AL-2s)
38	83	5.1	1206	1 W47030	Bovine N-proteins
39	83	5.1	396	1 W53868	Gravlin polypeptide
40	83	5.1	651	1 W53875	Gravlin polypeptide
41	83	5.1	1780	1 W53863	Human gravlin poly
42	83	5.1	453	1 W53867	Gravlin polypeptide
43	83	5.1	648	1 W62220	Raf-1 protein. Det

44 83 5.1 648 1 W30664
45 83 5.1 648 1 W95611

Human c-Raf-1 prot
Homo sapiens GST-R

ALIGNMENTS

RESULT 1

ID R97978 standard: Protein; 251 AA.

AC R97978; (first entry)

DE Stannocalcin alpha; heart disease; osteoporosis; hypocalcaemia;

KW renal disease; bone disease; Paget's disease; diagnosis;

OS Homo sapiens.

PN W09615147-A1;

PD 23-MAY-1996.

PE 10-NOV-1994; U13206.

PR 10-NOV-1994; WO-U13206.

PA (HMA-) HUMAN GENOME SCI INC.

PI Fleischmann RD, Olsen H;

DR WPI: 96-259780/26.

DR N-PSDB; 118979.

PT Human stannocalcin-alpha DNA and protein - useful for treatment and

PS diagnosis of electrolyte disorders leading to renal, heart and bone

CC diseases esp. osteoporosis and Paget's disease

CC Claim 1; Figure 1; 54pp; English.

CC The stannocalcin alpha polypeptide may be used for the treatment of

CC electrolyte disorders which lead to renal, bone and heart diseases,

CC polypeptide may be used therapeutically to treat hypocalcaemia and

CC osteoporosis. The stannocalcin alpha coding sequence may be used

CC in the detection of disease or to detect the susceptibility of

CC disease related to a mutated stannocalcin alpha coding sequence.

Sequence 251 AA;

Query Match 78.4%; Score 1271; DB 1; Length 251;

Best Local Similarity 94.9%; Pred. No. 3.3e-118;

Matches 240; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 MCAERLQGFMTALVATFDPAAGTATPPGPDSSQKGRISLQNTAEIOHCLVNA 60

DB 1 MCAERLQGFMTALVATFDPAAGTATPPGPDSSQKGRISLQNTAEIOHCLVNA 60

QY 61 GDVGCVFECFENNCEIRGLGICMTFLHNAKFPDAQGSFIDALKCAHAAHRHFGC 120

DB 61 GDVGCVFECFENNCEIRGLGICMTFLHNAKFPDAQGSFIDALKCAHAAHRHFGC 120

QY 121 ISKCPAIREMSVQRCRECYLKHDCAAAGENTRIYEMIFKDLLEHYVDLVNLLT 180

DB 121 ISKCPAIREMSVQRCRECYLKHDCAAAGENTRIYEMIFKDLLEHYVDLVNLLT 180

QY 181 CSEEVKEATHTSVQVCQNNNGSLISIFCTSAIQRPAPPEPOVDRTLSRAHNG 240

DB 181 CSEEVKEATHTSVQVCQNNNGSLISIFCTSAIQRPAPPEPOVDRTLSRAHNG 240

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253

QY 241 EAGHLLPESSRE 253

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QY 241 EAGHLLPESSRE 253

DB 241 EAGHLLPESSRE 253